PATENT APPLICATION

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE HONORABLE BOARD OF PATENT APPEALS AND INTERFERENCES

In re the Application of:

Glaucia PARANHOS-BACCALA et al.

Application No.: 09/138,735

Filed: August 24, 1998 Docket No.: WPB 36400B

For: TRYPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND METHOD OF DETECTING AND TREATING CHAGAS DISEASE

BRIEF ON APPEAL

Appeal from Group 1600

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I. Introduction

This is an Appeal from a Final Rejection mailed February 26, 2003, finally rejecting claims 5, 7, 8, 10-27, 32, 34 and 36-42. Claims 1 and 2 are allowed.

A. Real Party In Interest

The real party in interest for this Appeal and the present application is Bio Merieux, by way of an assignment recorded in the U.S. Patent and Trademark Office starting at Reel 7626, Frame 0182.

B. Statement of Related Appeals and Interferences

There are presently no appeals or interferences, known to Appellants, Appellants' representative or the Assignee, which will directly affect or be directly affected by or have a bearing upon the Board's decision in the pending appeal.

C. Status of Claims

Claims 1, 2, 5, 7, 8, 10-27, 32, 34, and 36-42 are pending. Claims 1 and 2 are allowed. Claims 5, 7, 8, 10-27, 32, 34 and 36-42 stand rejected and are on appeal. All of the pending claims are set forth in Appendix A.

Allowed claim 1 and rejected claims 5, 8, 21-23 and 27 are independent. Allowed claim 2 depends on allowed claim 1. Of the rejected claims, claims 7, 11-20, 25, 26, 32, 34, 39 and 41 ultimately depend from claim 5; claims 10, 40 and 42 depend from claim 8; claim 36 depends from claim 21; claim 37 depends from claim 22; and claims 24 and 38 depend from claim 23.

D. Status of Amendment

An Amendment After Final Rejection was filed on August 22, 2003. By an Advisory Action mailed October 3, 2003, the Examiner indicated that the amendments in this Amendment After Final Rejection have been entered. (Although the Advisory Action incorrectly refers to an Amendment After Final Rejection and a Notice of Appeal filed

September 8, 2003, it is respectfully submitted that these documents were timely filed on August 22, 2003, as indicated in the postcard receipt that was faxed to the Patent Office with copies of the documents on September 16, 2003.)

II. The Invention

Trypanosoma cruzi is a flagellate protozoal parasite and is responsible for Chagas disease, which affects millions of people, mainly in Latin America. Specification, page 1, lines 6-10. In vertebrate hosts, Trypanosoma cruzi is present in two forms. One of these forms is mobile by means of flagellum or trypomastigote and does not divide. The other form is aflagellate, or intracellular amastigote, which multiplies by binary division. Page 1, lines 11-15.

Transmission of the protozoan in man occurs through hematophagous insects of the family Reduviidae during a blood meal followed by dejections at the site of the bite. The vector insect thus releases the infectious metacyclic trypomastigote forms, which will colonize many cell types through blood circulation. Trypanosoma cruzi infects cardiac and skeletal muscular cells, the glial cells and the cells of the mononuclear phagocytic system. After passive penetration into the host cell, the trypomastigote form of the parasite differentiates into the amastigote form, divides actively and then is followed by a release of the trypomastigote forms, thereby causing a new cell invasion. Page 1, lines 16-29.

Two phases of Chagas disease can be distinguished: the acute phase and the chronic phase. The acute phase occurs after a transfusional, congenital or vectorial type contamination and last for a few weeks. It is characterized by a large number of parasites circulating in the blood and corresponds to an exponential division of the protozoan. The acute phase is most often asymptomatic. However, in infants contaminated by their mothers, the acute phase, which is marked by an acute cardiopathy, may be critical. The chronic phase may extend over many years. In some individuals, this phase is asymptomatic. However,

other patients have tissue lesions in the heart or digestive type manifestations. Page 2, lines 4-17.

Because of contamination through blood transfusion, this disease is becoming a worldwide problem. It is therefore becoming essential to have available diagnostic tests that make it possible to determine the presence of the parasite in individuals. Page 2, lines 21-25.

The present inventors have identified and obtained for the first time a new genetic material encoding a new protein, recognized by anti-Trypanosoma cruzi antisera. This genetic material, which the inventors have called Tc 100 and is identified in the application by SEQ ID NO: 1, may be used to produce proteins or polypeptides for the production of diagnostic tests or may itself be used as a probe or for the determination of specific probes that can be used in nucleic acid hybridization tests for the detection of Trypanosoma cruzi infections. In addition, the inventors have identified several fragments of SEQ ID NO: 1, specifically the fragment from nucleotides 1232 to 2207 of SEQ ID NO: 1 and even shorter fragments thereof. Page 4, lines 7-32, and page 7, lines 5-14. As described in the specification, fragments of these sequences and sequences having 85% homology therewith, specifically sequences having 85% homology with any succession of 30 monomers thereof, can be used as probes for identifying Trypanosoma cruzi. In addition, such sequences can be used as a primer for amplifying a nucleotide sequence. Page 7, lines 5-19; page 15, line 15 to page 17, line 21.

III. The Applied Reference

The applied reference is: U.S. Patent No. 5,302,527 to Birkett et al. (hereinafter "Birkett").

IV. Issues

There are three issues on appeal. The first issue is whether the present specification enables the subject matter recited in claims 5, 7, 8, 10-26, 32, 34 and 36-42, as required by

35 U.S.C. §112, first paragraph. The second issue on appeal is whether the present specification provides written description for claims 5, 7, 8, 10-27, 32, 34 and 36-42, as required by 35 U.S.C. §112, first paragraph. The third issue on appeal is whether claims 5, 8, 10, 11, 17, 25, 26, 32, 34, 39 and 40 are anticipated under 35 U.S.C. §102(b) by Birkett.

The rejection of claims 41 and 42 under 35 U.S.C. §112, first paragraph, raised in the February 26, 2003 Final Rejection was withdrawn in the October 3, 2003 Advisory Action. Thus, this is not an issue on appeal.

V. Grouping of Claims

Each claim of this Patent Application is separately patentable, and upon issuance of a patent will be entitled to a separate presumption of validity under 35 U.S.C. §282. For convenience in handling of this Appeal, the claims will be argued in 18 groups as follows:

Group I: Claims 21-23;

Group II: Claims 36-38;

Group III: Claim 24;

Group IV: Claim 8;

Group V: Claim 42;

Group VI: Claim 40;

Group VII: Claim 10;

Group VIII: Claim 5;

Group IX: Claims 41 and 7;

Group X: Claim 39;

Group XI: Claim 25;

Group XII: Claim 26;

Group XIII: Claim 11;

Group XIV: Claims 12-16;

Group XV: Claims 17 and 32;

Group XVI: Claims 18-20;

Group XVII: Claim 34; and

Group XVIII: Claim 27.

Thus, pursuant to 37 C.F.R. §1.192(c)(7), in this Appeal, the rejected claims within each Group will stand or fall together. However, the rejected claims of each Group do not stand or fall together with the rejected claims of any other Group. The rejected claims are grouped together in Appendix B.

VI. Argument

Claims 5, 7, 8, 10-26, 32, 34 and 36-42 are rejected under 35 U.S.C. §112, first paragraph, as allegedly containing subject matter that was not described in the specification in such a way as to enable one skilled in the art to which it pertains or with which it is most nearly connected to make and/or use the invention. In addition, claims 5, 7, 8, 10-27, 32, 34 and 36-42 are rejected under 35 U.S.C. §112, first paragraph, as allegedly containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. Furthermore, claims 5, 8, 10, 11, 17, 25, 26, 32, 34, 39 and 40 are rejected under 35 U.S.C. §102(b) as being anticipated by Birkett. However, it is respectfully submitted that the present specification provides written description and enablement for the rejected claims. In addition, it is respectfully submitted that Birkett does not anticipate the invention of the rejected claims.

A. Birkett Does Not Teach The Invention of The Present Claims

Claims 5, 8, 10, 11, 17, 25, 26, 32, 34, 39 and 40 are rejected under 35 U.S.C. §102(b) as being anticipated by Birkett. Claims 7, 12-16, 18-24, 27, 36-38, 41 and 42 are not rejected on this basis. Thus, none of claims 7, 12-16, 18-24, 27, 36-38, 41 and 42 have been grouped

together with any of claims 5, 8, 10, 11, 17, 25, 26, 32, 34, 39 and 40. The claims rejected on this basis have been grouped as follows: claim 8 (Group IV); claim 40 (Group VI); claim 10 (Group VII); claim 5 (Group VIII); claim 39 (Group X); claim 25 (Group XI); claim 26 (Group XII); claim 11 (Group XIII); claims 17 and 32 (Group XV); and claim 34 (Group XVII). It is respectfully submitted that Birkett does not teach each and every feature of claims 8, 40, 10, 5, 39, 25, 26, 11, 17, 32 and 34.

1. Birkett Does Not Anticipate the Subject Matter of Group IV

Claim 8 of Group IV is directed to a primer for amplifying a nucleotide sequence. The primer of claim 8 consists essentially of a sequence having at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence. In addition, the primer of claim 8 contains at least 5 and no more than 30 nucleotides.

Birkett describes the use of a mixture of hexamer oligonucleotides in a kit called *Multiprime Kit* by Amersham for random priming. Col. 15, lines 24-28. Random hexamer kits contain a collection of some of the over 4000 conceivable hexamers. The Examiner admitted in the February 26, 2003 Office Action "that every conceivable sequence of six consecutive nucleotides is not contained within the kit disclosed by Birkett" (emphasis added).

Birkett does not recite that the *Multiprime Kit* contains a primer according to claim 8. Thus, it appears to be the Examiner's position that because claim 8 encompasses a large number of primers, this kit would inherently contain a primer according to claim 8. However, the Examiner's position is in clear contrast with inherency law, which has consistently held that to invalidate a claim based on inherency, inherency must be a necessary result and not merely a possible result. The mere fact that a certain thing may result from a given set of

circumstances is not enough. In re Oelrich, 666 F.2d 578, 581, 212 USPQ 323, 326 (CCPA 1981); Ex parte Keith and Turnquest, 154 USPQ 320, 321 (Bd. Pat. Appl. & Int. 1966). Thus, the fact that in any given random hexamer kit, there may be a primer according to claim 8 is not sufficient to anticipate claim 8.

In addition, it is noted that the Final Rejection and Advisory Action have greatly exaggerated the number of primers encompassed by claim 8. In particular, claim 8 does not encompass every primer that would hybridize to any part of SEQ ID NO: 1. In fact, claim 8 makes no reference to an ability to hybridize to SEQ ID NO: 1. Instead, claim 8 encompasses primers having 5 to 30 nucleotides, wherein the primer consists essentially of a sequence having at least 85% homology with nucleotides 1232 to 2207 of SEQ ID NO: 1 or the corresponding RNA sequence or full complements thereof. These primer would, of course, hybridize to SEQ ID NO: 1 or its complement, specifically at nucleotides 1232 to 2207 thereof. However, claim 8 does not encompass all sequences that hybridize to SEQ ID NO: 1.

For at least these reasons, Birkett does not teach each and every feature of claim 8. Therefore, the rejection of claim 8 under 35 U.S.C. §102(b) should be withdrawn.

2. Birkett Does Not Anticipate the Subject Matter of Group VI

Claim 40 of Group VI depends from claim 8 of Group IV. Therefore, claim 40 is not anticipated by Birkett for at least the reasons discussed above with regard to claim 8.

In addition, claim 40 further recites that the primer contains at least five contiguous nucleotides of "said nucleotide sequence." The recitation in claim 40 of "said nucleotide sequence" clearly refers to the nucleotide sequence of claim 8, which is a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence. Birkett does not teach, on its face or by inherency, that any of the hexamers in the *Multiprime Kit* contains at

least 5 consecutive nucleotides of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.

For at least these reasons, Birkett does not teach each and every feature of claim 40. Therefore, the rejection of claim 40 under 35 U.S.C. §102(b) should be withdrawn.

3. Birkett Does Not Anticipate the Subject Matter of Group VII

Claim 10 of Group VII depends from claim 8 of Group IV. Therefore, claim 10 is not anticipated by Birkett for at least the reasons discussed above with regard to claim 8.

In addition, claim 10 further recites that the primer consists essentially of a nucleotide sequence selected from the group consisting of SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10 and SEQ ID NO: 12, all of which contain at least 18 nucleotides and are therefore clearly not one of the random hexamers contained in the kit described in Birkett.

For at least these reasons, Birkett does not teach each and every feature of claim 10. Therefore, the rejection of claim 10 under 35 U.S.C. §102(b) should be withdrawn.

4. Birkett Does Not Anticipate the Subject Matter of Group VIII

Claim 5 of Group VIII is directed to a probe for identifying Trypanosoma cruzi. The probe of claim 5 consists essentially of a sequence having at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence. In addition, the probe of claim 5 contains at least 5 and no more than 100 nucleotides.

As discussed above with regard to claim 8, Birkett describes the use of a mixture of hexamer oligonucleotides in a kit called *Multiprime Kit* by Amersham for random priming. Col. 15, lines 24-28. The Examiner admitted in the February 26, 2003 Office Action "that

every conceivable sequence of six consecutive nucleotides is not contained within the kit disclosed by Birkett" (emphasis added).

Birkett does not recite that the *Multiprime Kit* contains a probe according to claim 5. Thus, it appears to be the Examiner's position that because claim 5 encompasses a large number of primers, this kit would inherently contain a primer that has the features of a probe according to claim 8. However, the Examiner's position is in clear contrast with inherency law, which has consistently held that to invalidate a claim based on inherency, inherency must be a necessary result and not merely a possible result. The mere fact that a certain thing may result from a given set of circumstances is not enough. In re Oelrich, 666 F.2d 578, 581, 212 USPQ 323, 326 (CCPA 1981); Ex parte Keith and Turnquest, 154 USPQ 320, 321 (Bd. Pat. Appl. & Int. 1966). Thus, the fact that in any given random hexamer kit, there may be a primer that has the features of a probe according to claim 5 is not sufficient to anticipate claim 5.

In addition, it is noted that the Final Rejection and Advisory Action have greatly exaggerated the number of probes encompassed by claim 5. In particular, claim 5 does not encompass every probe that would hybridize to any part of SEQ ID NO: 1. In fact, claim 5 makes no reference to an ability to hybridize to SEQ ID NO: 1. Instead, claim 5 encompasses probes having 5 to 100 nucleotides, wherein the probe consists essentially of a sequence having at least 85% homology with nucleotides 1232 to 2207 of SEQ ID NO: 1 or the corresponding RNA sequence or full complements thereof. These probe would, of course, hybridize to SEQ ID NO: 1 or its complement, specifically at nucleotides 1232 to 2207 thereof. However, claim 5 does not encompass all sequences that hybridize to SEQ ID NO: 1.

For at least these reasons, Birkett does not teach each and every feature of claim 5. Therefore, the rejection of claim 5 under 35 U.S.C. §102(b) should be withdrawn.

5. Birkett Does Not Anticipate the Subject Matter of Group X

Claim 39 of Group X depends from claim 5 of Group VIII. Therefore, claim 39 is not anticipated by Birkett for at least the reasons discussed above with regard to claim 5.

In addition, claim 39 further recites that the probe contains at least five contiguous nucleotides of "said nucleotide sequence." The recitation in claim 39 of "said nucleotide sequence" clearly refers to the nucleotide sequence of claim 5, which is a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence. Birkett does not teach, on its face or by inherency, that any of the hexamers in the *Multiprime Kit* contains at least 5 consecutive nucleotides of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.

For at least these reasons, Birkett does not teach each and every feature of claim 39. Therefore, the rejection of claim 39 under 35 U.S.C. §102(b) should be withdrawn.

6. Birkett Does Not Anticipate the Subject Matter of Group XI

Claim 25 of Group XI depends from claim 5 of Group VIII. Therefore, claim 25 is not anticipated by Birkett for at least the reasons discussed above with regard to claim 5.

In addition, claim 25 further recites that "said nucleotide sequence is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence." Thus, claim 25 is directed to a probe having 5 to 100 nucleotides, wherein the probe consists essentially of a sequence having at least 85% homology with a narrower nucleotide range of SEQ ID NO: 1 or the corresponding RNA sequence or full complements thereof than is recited in claim 5. Specifically, this narrower range is from nucleotides 1232 to 1825. Birkett does not teach, on its face or by inherency, that any of the hexamers in the *Multiprime Kit* consists essentially of a sequence

having at least 85% homology with this narrower range of SEQ ID NO: 1 or the corresponding RNA sequence or full complements thereof.

For at least these reasons, Birkett does not teach each and every feature of claim 25. Therefore, the rejection of claim 25 under 35 U.S.C. §102(b) should be withdrawn.

7. Birkett Does Not Anticipate the Subject Matter of Group XII

Claim 26 of Group XII depends from claim 5 of Group VIII. Therefore, claim 26 is not anticipated by Birkett for at least the reasons discussed above with regard to claim 5.

In addition, claim 26 further recites that "said nucleotide sequence is identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence." Thus, claim 26 is directed to a probe having 5 to 100 nucleotides, wherein the probe consists essentially of a sequence having at least 85% homology with a narrower nucleotide range of SEQ ID NO: 1 or the corresponding RNA sequence or full complements thereof than is recited in claim 5. Specifically, this narrower range is from nucleotides 1266 to 2207. Birkett does not teach, on its face or by inherency, that any of the hexamers in the *Multiprime Kit* consists essentially of a sequence having at least 85% homology with this narrower range of SEQ ID NO: 1 or the corresponding RNA sequence or full complements thereof.

For at least these reasons, Birkett does not teach each and every feature of claim 26. Therefore, the rejection of claim 26 under 35 U.S.C. §102(b) should be withdrawn.

8. Birkett Does Not Anticipate the Subject Matter of Group XIII

Claim 11 of Group XIII is directed to a reagent for determining or identifying Trypanosoma cruzi in a biological sample. The reagent of claim 11 comprises both a capture probe and a detection probe having nucleotide sequences that are different from one another. As recited in claim 11, both of these probes are in accordance with claim 5 of Group VIII.

Therefore, claim 11 is not anticipated by Birkett for at least the reasons discussed above with regard to claim 5.

In addition, the reagent of claim 11 comprises two probes according to claim 5, one for capture and the other for detection, wherein the nucleotide sequences of these two probes are different. Birkett does not teach, on its face or by inherency, that any of the hexamers in the *Multiprime Kit* has the features of a probe according to claim 5, much less that the kit contains two such probes. To invalidate a claim based on inherency, inherency must be a necessary result and not merely a possible result. The mere fact that a certain thing may result from a given set of circumstances is not enough. In re Oelrich, 666 F.2d 578, 581, 212 USPQ 323, 326 (CCPA 1981); Ex parte Keith and Turnquest, 154 USPQ 320, 321 (Bd. Pat. Appl. & Int. 1966). Thus, the fact that in any given random hexamer kit, there may be two different primers that have the features of probes according to claim 5 is not sufficient to anticipate claim 11.

For at least these reasons, Birkett does not teach each and every feature of claim 11. Therefore, the rejection of claim 11 under 35 U.S.C. §102(b) should be withdrawn.

9. Birkett Does Not Anticipate the Subject Matter of Group XV

Claim 17 of Group XV depends from claim 11 of Group XIII. Claim 32 of Group XV depends on claim 17. Therefore, claims 17 and 32 are not anticipated by Birkett for at least the reasons discussed above with regard to claim 11.

In addition, claim 17 (and therefore claim 32 by it dependency on claim 17) further recites that the reagent further comprises at least one primer consisting essentially of a segment of at least five contiguous nucleotides of a nucleic acid that is identical or fully complementary to a first sequence starting a nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence. Birkett does not teach, on its face or by inherency, that any of the hexamers in the *Multiprime Kit* consists essentially of a segment of

at least five contiguous nucleotides of a nucleic acid that is identical or fully complementary to a first sequence starting a nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence, or that the *Multiprime Kit* contains such a hexamer in addition to the two probes discussed above with regard to claim 11.

For at least these reasons, Birkett does not teach each and every feature of claims 17 and 32. Therefore, the rejection of claim 17 and 32 under 35 U.S.C. §102(b) should be withdrawn.

10. Birkett Does Not Anticipate the Subject Matter of Group XVII

Claim 34 of Group XVII depends on claim 20 of Group XVI, which depends on claim 18 also of Group XVI, neither of claims 20 and 18 being rejected on this basis. Claim 18 is directed to a method for detection and/or identification of Trypanosoma cruzi in a biological sample, comprising exposing denatured DNA extracted from Trypanosoma cruzi or DNA obtained by reverse transcription of RNA extracted from Trypanosoma cruzi to at least one probe according to claim 5; and detecting hybridization of the probe. Claim 20 further recites that, before the DNA is exposed to the probe, the DNA is amplified with at least one primer. Claim 34 of Group XVII further defines this primer. Birkett does not teach a method for detection and/or identification of Trypanosoma cruzi in a biological sample, much less the specific method of claim 34.

For at least these reasons, Birkett does not teach each and every feature of claim 34. Therefore, the rejection of claim 34 under 35 U.S.C. §102(b) should be withdrawn.

11. Conclusion

Birkett does not teach each and every feature of claims 8, 40, 10, 5, 39, 25, 26, 11, 17, 32 and 34. Therefore, the rejection of these claims under 35 U.S.C. §102(b) should be withdrawn.

B. The Specification Enables the Present Claims

Claims 5, 7, 8, 10-26, 32, 34 and 36-42 are rejected under 35 U.S.C. §112, first paragraph, as allegedly containing subject matter that was not described in the specification in such a way as to enable one skilled in the art to which it pertains or with which it is most nearly connected to make and/or use the invention. The rejection of claim 27 on this basis was withdrawn in the October 3, 2003 Advisory Action.

Any analysis of whether a particular claim is supported by the disclosure in an application requires a determination of whether the disclosure, when filed, contained sufficient information regarding the subject matter of the claims as to enable one skilled in the pertinent art to make and use the claimed invention without undue experimentation. In re Wands, 858 F.2d 731, 737, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988). The fact that experimentation may be complex does not necessarily make it undue, if the art typically engages is such experimentation. The test of enablement is not whether any experimentation is necessary, but whether, if experimentation is necessary, it is undue. In re Angstadt, 537 F.2d 498, 504, 190 USPQ 214, 219 (CCPA 1976).

The presence or absence of working examples is only one factor in determining whether a claim is enabled. Other factors include: the breadth of the claim; the nature of the invention; the state of the prior art; the level of one of ordinary skill; the level of predictability in the art; the amount of direction provided by the inventor; and the quantity of experimentation needed to make or use the invention based on the content of the disclosure. Wands, 858 F.2d at 737, 8 USPQ2d at 1404. A lack of working examples does not by itself render a claim non-enabled.

Furthermore, in order to make an enablement rejection, the Examiner has the initial burden to establish a reasonable basis to question the enablement provided by the claimed

invention. In re Wright, 999 F.2d 1557, 1562, 27 USPQ2d 1510, 1513 (Fed. Cir. 1993). As stated by the court:

> It is incumbent upon the Patent Office, whenever a rejection on this basis is made, to explain *why* it doubts the truth or accuracy of any statement in a supporting disclosure and to back up assertions of its own with acceptable evidence or reasoning which is inconsistent with the contested statement. Otherwise, there would be no need for the applicant to go to the trouble and expense of supporting his presumptively accurate disclosures.

In re Marzocchi, 439 F.2d 220, 224, 169 USPQ 367, 370 (CCPA 1971).

It is respectfully submitted that based on this standard the present specification enables the subject matter of Claims 5, 7, 8, 10-26, 32, 34 and 36-42.

1. The Specification Enables The Subject Matter of Group I

Claims 21-23 of Group I are each independent claims directed to a synthetic or isolated nucleic acid fragment consisting of a nucleotide sequence having at least 85% homology with a reference sequence, wherein each segment of 30 contiguous nucleotides of the nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of the reference sequence. In each of claims 21-23, the reference sequence is a specific portion of SEQ ID NO: 1, the corresponding RNA sequence or full complements thereof. In claim 21, the portion is from nucleotides 1232 to 1825; in claim 22, the portion is from nucleotides 1232 to 2207; and in claim 23, the portion is from nucleotides 1266 to 2207. Thus, claims 21-23 encompass nucleic acids that consist of these portions, respectively, or sequences having at least 85% homology therewith, specifically where each segment of 30

contiguous nucleotides of the nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of the respective portion.

It is respectfully submitted that, at the time of the present invention, one of ordinary skill in the art would have been able to make and use the nucleic acids of claims 21-23 without undue experimentation. Specifically, one of ordinary skill in the art would have been able to use these sequences as probes or primers or to generate probes and primers for the identification or amplification, respectively, of Trypanosoma cruzi nucleic acids. In particular, it was well know in the art that nucleic acids having less than 100% homology with the complement of the target can be used as a probe or primer. Specifically, it was well known in the art that under appropriate hybridization conditions, a probe or primer sequence can hybridize to the complement of a sequence that has only 85% homology with the probe or primer sequence. Although the use of lower stringency conditions may increase the likelihood that the sequence binds to other molecules of unknown function and unknown origin, one of ordinary skill in the art can employ the use of additional probes and/or other techniques to confirm the identity of the identified or amplified sequence. Such experimentation was routine in the art and would not have been considered undue experimentation.

In rejecting the claims on this basis, the Patent Office indicates for the first time in the October 3, 2003 Advisory Action that the present specification does not enable claims reciting 85% homology because changing any nucleotide "results in a probe/primer which will now bind to other molecules of unknown function and unknown origin." The Patent Office cites no basis for this statement, nor does it explain why this would render the claims non-enabled. As discussed above, the use of a probe or primer have less than 100% homology with the complement of the target may necessitate the use of lower stringency conditions and therefore provide a greater chance that the probe or primer will bind to other

molecules of unknown function and unknown origin. However, this does not mean that the probes and primers cannot effectively be used. For example, other probes can be used to verify the identity of the sequence identified by the initial probe or amplified by the primer. The Patent Office has not provided any evidence or reasoning to suggest that such probes and primers cannot effectively be used.

The present specification enables the subject matter of claims 21-23. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of non-enablement of claims 21-23. Therefore, the enablement rejection of claims 21-23 under 35 U.S.C. §112, first paragraph, should be withdrawn.

2. The Specification Enables The Subject Matter of Group II

Claims 36-38 of Group II depend, respectively, from claims 21-23 of Group I. Thus, claims 36-38 are enabled by the present specification for at least the reasons discussed above with regard to claims 21-23.

In addition, claims 36-38 each further define the nucleotide sequences of claims 21-23, respectively, as being identical to or a degenerate of the sequence referred to as the "reference sequence" in claims 21-23. Thus, claims 36-38 are directed to a nucleic acid fragment consisting of: (1) a nucleic acid sequence that is identical to or is a degenerate of a specifically defined portion of SEQ ID NO: 1 or the corresponding RNA sequence, or (2) a full complement of a nucleic acid sequence that is identical to or is a degenerate of a specifically defined portion of SEQ ID NO: 1 or the corresponding RNA sequence. In claim 36, the specifically defined portion is from nucleotides 1232 to 1825; in claim 37, the specifically defined portion is from nucleotides 1232 to 2207; and in claim 38, the specifically defined portion is from nucleotides 1266 to 2207.

In addition to using these sequences as a probe or primer or to generate probes and primers, the sequences of claims 36-38 can also be used to form the peptide sequence

encoded by the claimed portions of SEQ ID NO: 1. As discussed throughout the specification, such peptide sequences can also be used in the diagnosis of Trypanosoma cruzi. The Patent Office has provided no basis to support the determination that claims 36-38 are not enabled.

The present specification enables the subject matter of claims 36-38. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of non-enablement of claims 36-38. Therefore, the enablement rejection of claims 36-38 under 35 U.S.C. §112, first paragraph, should be withdrawn.

3. The Specification Enables The Subject Matter of Group III

Claim 24 of Group III depends on claim 23 of Group I. Thus, claim 24 is enabled by the present specification for at least the reasons discussed above with regard to claim 23.

In addition, claim 24 further defines the nucleotide sequence of claim 23 as being identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence. Thus, claim 24 is directed to a nucleic acid fragment consisting of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence. The Patent Office cites no basis to support the determination that claim 24 is not enabled.

The present specification enables the subject matter of claim 24. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of non-enablement of claim 24. Therefore, the enablement rejection of claim 24 under 35 U.S.C. §112, first paragraph, should be withdrawn.

4. The Specification Enables The Subject Matter of Group IV

Claim 8 of Group IV is an independent claim directed to a primer for amplifying a nucleotide sequence. In claim 8, the primer consists essentially of a sequence having at least

85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence. In addition, claim 8 further defines the primer as containing at least 5 and no more than 30 nucleotides.

It is respectfully submitted that, at the time of the present invention, one of ordinary skill in the art would have been able to make and use the primers of claim 8 without undue experimentation. Specifically, one of ordinary skill in the art would have been able to use these sequences to amplify Trypanosoma cruzi nucleic acids. In particular, it was well know in the art at that time that sequences having less than 100% homology with the complement of the target can be used as a primer. Specifically, it was well known in the art that under appropriate hybridization conditions, a primer sequence can hybridize to the complement of a sequence that has only 85% homology with the primer sequence. Although the use of lower stringency conditions may increase the likelihood that the sequence binds to other nucleic acids, a second primer is generally used in an amplification reaction, which will decrease the likelihood of non-specific amplification. In addition, one of ordinary skill in the art could employ the use of techniques to confirm the identity of the amplified sequence. Such experimentation was at the time routine in the art and would not have been considered undue experimentation.

In rejecting the claims on this basis, the Patent Office indicates for the first time in the October 3, 2003 Advisory Action that the present specification does not enable claims reciting 85% homology because changing any nucleotide "results in a probe/primer which will now bind to other molecules of unknown function and unknown origin." The Patent Office cites no basis for this statement, nor does it explain why this would render the claims non-enabled. As discussed above, the use of a primer have less than 100% homology with the complement of the target may necessitate the use of lower stringency conditions and

therefore provide a greater chance that the primer will bind to other nucleic acids. However, this does not mean that the primers cannot effectively be used. The Patent Office has not provided any evidence or reasoning to suggest that such primers cannot effectively be used.

The Patent Office also argues that use of "consisting essentially of" language renders the claims non-enabled. However, it is respectfully submitted that one of ordinary skill in the art at the time was well aware that additional matter could be added to a primer without affecting the basic and novel characteristics of that primer. For example, it may be possible to add one or more additional nucleotides to one or more ends of a primer without affecting the basic and novel characteristics of that primer. In addition, to the extent that adding something would effect the basic and novel characteristics of the primer, its addition is excluded by the "consisting essentially of" language.

The Patent Office argues, however, that the phrase "consisting essentially of" is being construed as equivalent to "comprising" since there is allegedly not a clear indication in the specification or claims of what the basic and novel characteristics actually are. It is respectfully submitted that it is clear from the claims and specification that the basic and novel characteristics of the invention of claim 8 is the ability of these sequences to hybridize and therefore act as a primer for amplifying Trypanosoma cruzi nucleotide sequences. Thus, the "consisting essentially of" language does have meaning in the context of claim 8.

In addition, it is respectfully submitted that even if claim 8 is incorrectly construed as having language equivalent to "comprising" language, claim 8 is still enabled by the present specification. In particular, use of the term "comprising" has consistently been allowed despite the fact that in all technologies it opens the claims to the inclusion of elements that could have a negative impact on the ability of the recited elements to function for their intended purpose. The fact that "comprising" language is open-ended does not create an enablement issue. Instead, based on the present disclosure, one of ordinary skill in the art

would have been able to practice the invention without undue experimentation. In particular, if one of ordinary skill in the art chooses to add nucleotides up and/or downstream of the recited sequence, he or she would need to test the ability of the modified sequence to act as a primer. However, such experimentation would have been considered routine in the art at the time of the present invention. Therefore, claim 8 is enabled by the present specification.

The present specification enables the subject matter of claim 8. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of non-enablement of claim 8. Therefore, the enablement rejection of claim 8 under 35 U.S.C. §112, first paragraph, should be withdrawn.

5. The Specification Enables The Subject Matter of Group V

Claim 42 of Group V depends from claim 8 of Group IV. Thus, claim 42 is enabled by the present specification for at least the reasons discussed above with regard to claim 8.

In addition, claim 42 further recites that the primer has 7 to 30 nucleotides. It is respectfully submitted that, at the time of the present invention, one of ordinary skill in the art would have been able to make and use primers having 7 to 30 nucleotides without undue experimentation. In particular, at the time of the present invention, it was well known in the art that primers having at least 7 nucleotides could be effectively used to amplify a target sequence. In the present application, specific sequences of Trypanosoma cruzi nucleic acid have been identified. Therefore, based on this teaching, one of ordinary skill in the art would have been able to select sequences having at least 7 nucleotides in order to amplify these Trypanosoma cruzi nucleic acids without undue experimentation.

The present specification enables the subject matter of claim 42. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of non-enablement of claim 42. Therefore, the enablement rejection of claim 42 under 35 U.S.C. §112, first paragraph, should be withdrawn.

6. The Specification Enables The Subject Matter of Group VI

Claim 40 of Group VI depends from claim 8 of Group IV. Thus, claim 42 is enabled by the present specification for at least the reasons discussed above with regard to claim 8.

In addition, claim 40 further defines the primer as containing at least 5 contiguous nucleotides of the nucleotide sequence. Thus, the primer of claim 40 contains at least 5 contiguous nucleotides of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.

It is respectfully submitted that, at the time of the present invention, one of ordinary skill in the art would have been able to make and use primers having at least 5 contiguous nucleotides of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence. In particular, it was well known in the art that primers having 5 contiguous nucleotides identical to the complement of the target sequence could be effectively used to amplify a target sequence. Thus, at the time of the present invention, one of ordinary skill in the art would have been able to make and use the primer of claim 40 to amplify Trypanosoma cruzi nucleic acids without undue experimentation.

The present specification enables the subject matter of claim 40. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of non-enablement of claim 40. Therefore, the enablement rejection of claim 40 under 35 U.S.C. §112, first paragraph, should be withdrawn.

7. The Specification Enables The Subject Matter of Group VII

Claim 10 of Group VII depends from claim 8 of Group IV. Thus, claim 10 is enabled by the present specification for at least the reasons discussed above with regard to claim 8.

In addition, claim 10 further defines the primer as consisting essentially of a nucleotide sequence selected from the group consisting of SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10 and SEQ ID NO: 12. It is respectfully submitted that, at the time of the present invention, one of ordinary skill in the art would have been able to make and use primers consisting essentially of one of these specifically identified sequences without undue experimentation. In particular, this claim does not recite sequences having at least 85% homology with a recited sequence. In addition, as discussed above with regard to claim 8, recitation of the transitional phrase "consisting essentially of" does not render claim 10 non-enabled.

The present specification enables the subject matter of claim 10. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of non-enablement of claim 10. Therefore, the enablement rejection of claim 10 under 35 U.S.C. §112, first paragraph, should be withdrawn.

8. The Specification Enables The Subject Matter of Groups VIII and XI-XVII

Claim 5 of Group VIII is an independent claim directed to probe for identifying Trypanosoma cruzi. In claim 5, the probe consists essentially of a sequence having at least 85% homology with a fragment of nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence. In addition, claim 5 recites that the probe contains at least 5 and no more than 100 nucleotides. Claim 25 of Group XI, claim 26 of Group XII, claim 11 of Group XIII, claims 12-16 of Group XIV, claims 17 and 32 of Group XV, claims 18-20 of Group XVI and claim 34 of Group XVII all depend, either directly or indirectly, from claim 5 of Group VIII, and the Patent Office does not set forth a separate basis for rejection of claims 25, 26, 11, 12-16, 17, 32, 18-20 and 34.

It is respectfully submitted that, at the time of the present invention, one of ordinary skill in the art would have been able to make and use the probes of claim 5 without undue experimentation. Specifically, one of ordinary skill in the art would have been able to use these probes to identify Trypanosoma cruzi nucleic acids. In particular, it was well know in the art at that time that a sequence having less than 100% homology with the complement of the target can be effectively used as a probe. Specifically, it was well known in the art that under appropriate hybridization conditions, a probe sequence can hybridize to the complement of a sequence that has only 85% homology with the probe sequence. Although the use of lower stringency conditions may increase the likelihood that the sequence binds to other nucleic acids, one of ordinary skill in the art could employ the use of other probes and/or techniques to confirm the identity of the identified sequence. Such experimentation was at the time routine in the art and would not have been considered undue experimentation.

In rejecting the claims on this basis, the Patent Office indicates for the first time in the October 3, 2003 Advisory Action that the present specification does not enable claims reciting 85% homology because changing any nucleotide "results in a probe/primer which will now bind to other molecules of unknown function and unknown origin." The Patent Office cites no basis for this statement, nor does it explain why this would render the claims non-enabled. As discussed above, the use of a probe have less than 100% homology with the complement of the target may necessitate the use of lower stringency conditions and therefore provide a greater chance that the probe will bind to other nucleic acids. However, this does not mean that the probes cannot effectively be used. The Patent Office has not provided any evidence or reasoning to suggest that such probes cannot effectively be used.

The Patent Office also argues that use of "consisting essentially of" language renders the claims non-enabled. However, it is respectfully submitted that one of ordinary skill in the art at the time was well aware that additional matter can be added to a probe without affecting

the basic and novel characteristics of that probe. For example, a label could be and at the time was routinely added to a probe without effecting the basic and novel characteristics of the probe. In addition, it may be possible to add one or more additional nucleotides to one or more ends of a probe without affecting the basic and novel characteristics of that probe. Furthermore, to the extent that adding something would effect the basic and novel characteristics of the probe, its addition is excluded by the "consisting essentially of" language.

The Patent Office argues, however, that the phrase "consisting essentially of" is being construed as equivalent to "comprising" since there is allegedly not a clear indication in the specification or claims of what the basic and novel characteristics actually are. It is respectfully submitted that it is clear from the claims and specification that the basic and novel characteristics of the invention of claim 5 is the ability of these sequences to hybridize and therefore act as a probe for identifying Trypanosoma cruzi nucleotide sequences. In particular, claim 5 specifically recites that the probe is "for identifying Trypanosoma cruzi." Thus, the "consisting essentially of" language does have meaning in the context of claim 5.

In addition, it is respectfully submitted that even if claim 5 is incorrectly construed as having language equivalent to "comprising" language, claim 5 is still enabled by the present specification. In particular, use of the term "comprising" has consistently been allowed despite the fact that in all technologies it opens the claims to the inclusion of elements that could have a negative impact on the ability of the recited elements to function for their intended purpose. The fact that "comprising" language is open-ended does not create an enablement issue. Instead, based on the present disclosure, one of ordinary skill in the art would have been able to practice the invention without undue experimentation. In particular, if one of ordinary skill in the art chooses to add nucleotides up and/or downstream of the recited sequence, he or she would need to test the ability of the modified sequence to act as a

probe. However, such experimentation would have been considered routine in the art at the time of the present invention. Therefore, claim 5 is enabled by the present specification.

The present specification enables the subject matter of claims 5. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of non-enablement of claim 5. Therefore, the enablement rejection under 35 U.S.C. §112, first paragraph, of claim 5 and of claims 25, 26, 11, 12-16, 17, 32, 18-20 and 34, which depend from claim 5, should be withdrawn.

9. The Specification Enables The Subject Matter of Group IX

Claims 41 and 7 of Group IX each depend from claim 5 of Group VIII. Thus, claims 41 and 7 are enabled by the present specification for at least the reasons discussed above with regard to claim 5.

In addition, claims 41 and 7 further define the probe as having from 7 to 100 nucleotides or from 8 to 50 nucleotides, respectively. It is respectfully submitted that, at the time of the present invention, one of ordinary skill in the art would have been able to make and use probes having 7 to 100 nucleotides or 8 to 50 nucleotides without undue experimentation. In particular, at the time of the present invention, it was well known in the art that primers having at least 7 or at least 8 nucleotides could be effectively used to amplify a target sequence. In the present application, specific nucleic acid sequences of Trypanosoma cruzi have been identified. Therefore, based on this teaching, one of ordinary skill in the art would have been able to select sequences having at least 7 or at least 8 nucleotides in order to identify these Trypanosoma cruzi nucleic acids without undue experimentation.

The present specification enables the subject matter of claims 41 and 7. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of non-enablement of claims 41 and 7. Therefore, the enablement rejection of claims 41 and 7 under 35 U.S.C. §112, first paragraph, should be withdrawn.

10. The Specification Enables The Subject Matter of Group X

Claim 39 of Group X depends from claim 5 of Group VIII. Thus, claim 39 is enabled by the present specification for at least the reasons discussed above with regard to claim 5.

In addition, claim 39 further defines the probe as containing at least 5 contiguous nucleotides of said nucleotide sequence. Thus, the probe of claim 39 contains at least 5 contiguous nucleotides of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.

It is respectfully submitted that, at the time of the present invention, one of ordinary skill in the art would have been able to make and use probes having at least 5 contiguous nucleotides of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence. In particular, it was well known in the art that probes having 5 contiguous nucleotides identical to the complement of the target sequence could be effectively used to identify a target sequence. Thus, at the time of the present invention, one of ordinary skill in the art would have been able to make and use the probe of claim 39 to identify Trypanosoma cruzi nucleic acids without undue experimentation.

The present specification enables the subject matter of claim 39. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of non-enablement of claim 39. Therefore, the enablement rejection of claim 39 under 35 U.S.C. §112, first paragraph, should be withdrawn.

11. Conclusion

The present specification enables the subject matter of claims 5, 7, 8, 10-26, 32, 34 and 36-42. Therefore, the enablement rejection under 35 U.S.C. §112, first paragraph, should be withdrawn.

C. The Specification Provides Written Description For The Present Claims

Claims 5, 7, 8, 10-27, 32, 34 and 36-42 are rejected under 35 U.S.C. §112, first paragraph, as allegedly containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention.

To provide written description for a claim, the specification as originally filed must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, the inventors were in possession of the invention as claimed. Vas-Cath, Inc. v. Mahurkar, 935 F.2d 1555, 1563-64, 19 USPQ2d 1111, 1117 (Fed. Cir. 1991). A written description requirement issue generally involves the question of whether the subject matter of a claim is supported by the disclosure of the application as filed. In the present case, the Examiner has not alleged that the claims are not supported by the language of the present specification. Instead, in alleging that the specification does not provide written description for the claims, the Examiner relies on a recent line of biotechnology cases that have held that merely identifying a nucleic acid by its principle biological activity, such as reciting a DNA that encodes a particular protein, does not provide written description for that compound.

Specifically, the Examiner relies on University of California v. Eli Lilly & Co., 119 F.3d 1559, 1566, 43 USPQ2d 1398, 1404 (Fed. Cir. 1997), which states that an adequate written description of a DNA "requires a precise definition, such as by structure, formula, chemical name, or physical properties, not a mere wish or plan for obtaining the claimed chemical invention." In Eli Lilly, the Federal Circuit held that a claim directed to human insulin cDNA was not adequately supported by the specification, which merely identified the cDNA by its principle biological activity, i.e., encoding human insulin, and a potential method for isolating it, without describing any structural features of the cDNA. 119 F.3d at 1567, 43 USPQ2d at 1404-05. In addition, the Federal Circuit held that the description of rat

insulin cDNA was insufficient to support claims that generically recite vertebrate or mammalian insulin cDNA, which would, of course, encompass human as well as rat cDNA. Eli Lilly, 119 F.3d at 1568, 43 USPQ2d at 1405. Thus, in Eli Lilly, the Federal Circuit held that providing no structural information about the claimed human DNA was insufficient. However, the Federal Circuit has not held that it is necessary to set forth an exact nucleotide sequence for any sequence within the claim, much less for more than one embodiment within a claim, in order to fulfill the written description requirement, as is suggested in the Final Rejection. In fact, Eli Lilly clearly supports the opposite conclusion stating that an adequate written description "requires a precise definition, such as by structure, formula, chemical name, or physical properties," clearly indicating that something other than the exact formula can be sufficient to precisely define and thus provide written description for a nucleic acid.

Instead, what is required for written description is a precise definition of the nucleic acid "sufficient to distinguish [the claimed material] from other materials." Eli Lilly, 119 F.3d at 1568, 43 USPQ2d at 1405. As discussed below, the present specification provides a precise definition of the claimed nucleic acid in a manner that is sufficient to distinguish the claimed nucleic acids from other nucleic acids.

In addition, a description as filed is presumed to be adequate, unless or until sufficient evidence or reasoning to the contrary has been presented by the Examiner to rebut the presumption. See, e.g., In re Marzocchi, 439 F.2d 220, 224, 169 USPQ 367, 370 (CCPA 1971). The Examiner, therefore, must have a reasonable basis to challenge the adequacy of the written description. Specifically, the Examiner has the initial burden of presenting by a preponderance of evidence why a person skilled in the art would not recognize in the specification a description of the invention defined by the claims. In re Wertheim, 541 F.2d 257, 262, 191 USPQ 90, 96 (CCPA 1976).

It is respectfully submitted that based on this standard the present specification provides written description for the subject matter of claims 5, 7, 8, 10-27, 32, 34 and 36-42.

1. The Specification Supports The Subject Matter of Group I

Claims 21-23 of Group I are each independent claims directed to a synthetic or isolated nucleic acid fragment consisting of a nucleotide sequence having at least 85% homology with a reference sequence, wherein each segment of 30 contiguous nucleotides of the nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of the reference sequence. In each of claims 21-23, the reference sequence is a specific portion of SEQ ID NO: 1, the corresponding RNA sequence or full complements thereof. In claim 21, the portion is from nucleotides 1232 to 1825; in claim 22, the portion is from nucleotides 1232 to 2207; and in claim 23, the portion is from nucleotides 1266 to 2207. Thus, claims 21-23 encompass nucleic acids that consist of these portions, respectively, or sequences having at least 85% homology therewith, specifically where each segment of 30 contiguous nucleotides of the nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of the respective portion.

Unlike the situation in Eli Lilly, the present specification clearly provides more than a mere statement that the claimed nucleotide sequences are part of the invention and reference to a potential method for isolating them. Instead, the specification clearly indicates that the inventors isolated and sequenced SEQ ID NO: 1 and identified the portions thereof recited in claims 21-23. Page 7, lines 5-14.

In addition to describing these specific sequences, the specification specifically describes nucleotide sequences having at least 85% homology with the recited sequences, particularly where each segment of 30 contiguous nucleotides of the nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of the respective portion. Page 7, lines 15-19. This reference to nucleotide sequences having at least 85% homology

with the recited sequences provides substantial structural information about all of the sequences within claims 21-23. In particular, the specification provides sufficient structural information to distinguish the claimed nucleic acids from nucleic acids that are outside the scope of the claims, as was required by the Federal Circuit in Eli Lilly. That is, even though the specification does not set forth the nucleotide sequence of every nucleic acid within the claims, one could easily identify by its nucleotide sequence whether a particular nucleic acid has at least 85% homology with the claimed portions of SEQ ID NO: 1, and whether each segment of 30 contiguous nucleotides of the nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of the respective portion, and is thus within the scope of claims 21-23. As a result, the present situation can be clearly distinguished from the situation in Eli Lilly where a nucleic acid was identified merely by its principle biological activity. Instead, in the present case, the claimed nucleic acids are identified by distinguishing structural characteristics.

For at least these reasons, it is respectfully submitted that the specification clearly supports claim 21-23. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of no written description with regard to claims 21-23. Therefore, the written description rejection of claims 21-23 under 35 U.S.C. §112, first paragraph, should be withdrawn.

2. The Specification Supports The Subject Matter of Group II

Claims 36-38 of Group II depend, respectively, from claims 21-23 of Group I. Thus, claims 36-38 are supported by the present specification for at least the reasons discussed above with regard to claims 21-23.

In addition, claims 36-38 each further define the nucleotide sequences of claims 21-23, respectively, as being identical to or a degenerate of the sequence referred to as the "reference sequence" in claims 21-23. Thus, claims 36-38 are directed to a nucleic acid

fragment consisting of: (1) a nucleic acid sequence that is identical to or is a degenerate of a specifically defined portion of SEQ ID NO: 1 or the corresponding RNA sequence, or (2) a full complement of a nucleic acid sequence that is identical to or is a degenerate of a specifically defined portion of SEQ ID NO: 1 or the corresponding RNA sequence. In claim 36, the specifically defined portion is from nucleotides 1232 to 1825; in claim 37, the specifically defined portion is from nucleotides 1232 to 2207; and in claim 38, the specifically defined portion is from nucleotides 1266 to 2207. Support for claims 36-38 can be found in the specification as filed at, for example, page 6, lines 26-29, which refers to nucleotide fragments "encoding a peptide . . . identical to the peptide encoded by the reference fragment." The Patent Office has not provided any basis to support the determination that the specification does not provide written description for claims 36-38.

For at least these reasons, it is respectfully submitted that the specification clearly supports claim 36-38. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of no written description with regard to claims 36-38. Therefore, the written description rejection of claims 36-38 under 35 U.S.C. §112, first paragraph, should be withdrawn.

3. The Specification Supports The Subject Matter of Group III

Claim 24 of Group III depends on claim 23 of Group I. Thus, claim 24 is supported by the present specification for at least the reasons discussed above with regard to claim 23.

In addition, claim 24 further defines the nucleotide sequence of claim 23 as being identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence. Thus, claim 24 is directed to a nucleic acid fragment consisting of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence. Claim 24 does not recite sequences

having 85% homology with the recited sequence. Thus, the Patent Office cites has not provided any basis for its determination that claim 24 is not supported by the present specification.

For at least these reasons, it is respectfully submitted that the specification supports claim 24. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of no written description with regard to claim 24. Therefore, the written description rejection of claim 24 under 35 U.S.C. §112, first paragraph, should be withdrawn.

4. The Specification Supports The Subject Matter of Groups IV-VI

Claim 8 of Group IV is an independent claim directed to a primer for amplifying a nucleotide sequence. In claim 8, the primer consists essentially of a sequence having at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence. In addition, claim 8 further defines the primer as containing at least 5 and no more than 30 nucleotides. Claim 42 of Group V and claim 40 of Group VI depend from claim 8 of Group IV, and the Patent Office does not set forth a separate basis for the rejection of claims 40 and 42.

Unlike the situation in Eli Lilly, the present specification clearly provides more than a mere statement that the claimed primers are part of the invention and reference to a potential method for isolating them. Instead, the specification clearly indicates that the inventors isolated and sequenced SEQ ID NO: 1 and identified the portion of SEQ ID NO: 1 recited in claim 8. Page 7, lines 5-14.

In addition to describing SEQ ID NO: 1 and the claimed portion thereof, the specification specifically describes primer sequences having at least 85% homology with SEQ ID NO: 1 and portions thereof. Page 15, lines 15-25; and page 17, lines 15-16. This reference to primer sequences having at least 85% homology with the SEQ ID NO: 1 and

portions thereof provides substantial structural information about all of the primer sequences encompassed by claim 8. In particular, the specification provides sufficient structural information to distinguish the claimed primers from nucleic acids that are outside the scope of the claims, as was required by the Federal Circuit in Eli Lilly. That is, even though the specification does not set forth the nucleotide sequence of every primer within claim 8, one of ordinary skill in the art could easily identify by its nucleotide sequence whether a particular primer has at least 85% homology with a sequence of the claimed portion of SEQ ID NO: 1, and is thus within the scope of the claim 8. As a result, the present situation can be clearly distinguished from the situation in Eli Lilly where a nucleic acid was identified merely by its principle biological activity. Instead, in the present case, the claimed primers are identified by distinguishing structural characteristics.

In rejecting the claims on this basis, the Patent Office objects to the transitional phrase "consisting essentially of." In particular, the Patent Office argues that the phrase "consisting essentially of" is being construed as equivalent to "comprising" since there is allegedly not a clear indication in the specification or claims of what the basic and novel characteristics actually are. It is respectfully submitted that it is clear from the claims and specification that the basic and novel characteristic of the invention of claim 8 is clearly the ability of these sequences to hybridize and therefore act as a primer for amplifying Trypanosoma cruzi nucleotide sequences. Thus, the "consisting essentially of" language does have meaning in the context of claim 8.

In addition, it is respectfully submitted that even if claim 8 is incorrectly construed as having language equivalent to "comprising" language, claim 8 is supported by the present specification. In particular, the original primer claims had "comprising" language. In addition, the recitation of open-ended "comprising" language does not by itself create a written description issue under the Eli Lilly line of cases. In particular, even if the inclusion

of additional nucleotides in a primer can have a "profound effect" on the activity of that primer, as alleged by the Patent Office, this does not mean that a claim containing open-ended "comprising" language lacks written description. The Patent Office has cited no basis for such a rejection.

Furthermore, based on the high level of skill in the art, it would be clear to one of ordinary skill in the art reading the specification that the inventors envisioned excluding things that would effect the basic and novel characteristics of the invention, specifically things that would have a detrimental effect on the ability of the nucleotide sequence to hybridize and therefore act as a primer for amplifying Trypanosoma cruzi nucleotide sequences. Thus, the "consisting essentially of" language is also supported by the present specification. Furthermore, it is respectfully submitted that this language excludes additional nucleotides that would have a "profound effect" on the activity of the primer, thereby alleviating the Examiner's concern regarding "comprising" language.

For at least these reasons, it is respectfully submitted that the specification supports claim 8. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of no written description with regard to claim 8. Therefore, the written description rejection under 35 U.S.C. §112, first paragraph, of claim 8, and of claims 42 and 40, which depend on claim 8, should be withdrawn.

5. <u>The Specification Supports The Subject Matter of Group VII</u>

Claim 10 of Group VII depends from claim 8 of Group IV. Thus, claim 10 is supported by the present specification for at least the reasons discussed above with regard to claim 8.

In addition, claim 10 further defines the primer as consisting essentially of a nucleotide sequence selected from the group consisting of SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10 and SEQ ID NO: 12. Claim 10 does not recite sequences having 85%

homology with the recited sequences. Thus, the only alleged basis for rejection of this claim is the inclusion of "consisting essentially of" language. As discussed above with regard to claim 8, the specification supports "consisting essentially of" language.

For at least these reasons, it is respectfully submitted that the specification supports claim 10. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of no written description with regard to claim 10. Therefore, the written description rejection of claim 10 under 35 U.S.C. §112, first paragraph, should be withdrawn.

6. The Specification Supports The Subject Matter of Groups VIII-XVII

Claim 5 of Group VIII is an independent claim directed to probe for identifying Trypanosoma cruzi. In claim 5, the probe consists essentially of a sequence having at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence. In addition, claim 5 recites that the probe contains at least 5 and no more than 100 nucleotides. Claims 41 and 7 of Group IX, claim 39 of Group X, claim 25 of Group XI, claim 26 of Group XII, claim 11 of Group XIII, claims 12-16 of Group XIV, claims 17 and 32 of Group XV, claims 18-20 of Group XVI and claim 34 of Group XVII all depend, either directly or indirectly, from claim 5 of Group VIII, and the Patent Office does not set forth a separate basis for the rejection of claims 41, 7, 39, 25, 26, 11, 12-16, 17, 32, 18-20 and 34.

Unlike the situation in Eli Lilly, the present specification clearly provides more than a mere statement that the claimed probes are part of the invention and reference to a potential method for isolating them. Instead, the specification clearly indicates that the inventors isolated and sequenced SEQ ID NO: 1 and identified the portion of SEQ ID NO: 1 recited in claim 5. Page 7, lines 5-14.

In addition to describing SEQ ID NO: 1 and the claimed portion thereof, the specification specifically describes probe sequences having at least 85% homology with SEQ ID NO: 1 and portions thereof. Page 15, lines 15-25. This reference to probe sequences having at least 85% homology with the SEQ ID NO: 1 and portions thereof provides substantial structural information about all of the probe sequences encompassed by claim 5. In particular, the specification provides sufficient structural information to distinguish the claimed probes from nucleic acids that are outside the scope of the claims, as was required by the Federal Circuit in Eli Lilly. That is, even though the specification does not set forth the nucleotide sequence of every probe within claim 5, one of ordinary skill in the art could easily identify by its nucleotide sequence whether a particular probe has at least 85% homology with a sequence of the claimed portion of SEQ ID NO: 1, and is thus within the scope of claim 5. As a result, the present situation can clearly be distinguished from the situation in Eli Lilly where a nucleic acid was identified merely by its principle biological activity. Instead, in the present case, the claimed probes are identified by distinguishing structural characteristics.

In rejecting the claims on this basis, the Patent Office objects to the transitional phrase "consisting essentially of." In particular, the Patent Office argues that the phrase "consisting essentially of" is being construed as equivalent to "comprising" since there is allegedly not a clear indication in the specification or claims of what the basic and novel characteristics actually are. It is respectfully submitted that it is clear from the claims and specification that the basic and novel characteristic of the invention of claim 5 is the ability of these sequences to hybridize and therefore act as a probe for identifying Trypanosoma cruzi nucleotide sequences. In fact, claim 5 specifically recites that the probe is for "identifying Trypanosoma cruzi." Thus, the "consisting essentially of" language does have meaning in the context of claim 5.

In addition, it is respectfully submitted that even if claim 5 is incorrectly construed as having language equivalent to "comprising" language, claim 5 is supported by the present specification. In particular, the original probe claims had "comprising" language. In addition, the specification specifically refers to the inclusion of a label in the probe, thus demonstrating possession of embodiments in which the probe contains more than the specifically recited sequence. Further, the recitation of open-ended "comprising" language does not by itself create a written description issue under the Eli Lilly line of cases. In particular, even if the inclusion of additional nucleotides in a probe can have a "profound effect" on the activity of that probe, as alleged by the Patent Office, this does not mean that a claim containing open-ended "comprising" language lacks written description. The Patent Office has cited no basis for such a rejection.

Furthermore, based on the high level of skill in the art, it would be clear to one of ordinary skill in the art reading the specification that the inventors envisioned excluding things that would effect the basic and novel characteristics of the invention, specifically things that would have a detrimental effect on the ability of the nucleotide sequence to hybridize and therefore act as a probe for amplifying Trypanosoma cruzi nucleotide sequences. Thus, the "consisting essentially of" language is also supported by the present specification. Furthermore, it is respectfully submitted that this language excludes additional nucleotides that would have a "profound effect" on the activity of the probe, thereby alleviating the Examiner's concern regarding "comprising" language.

For at least these reasons, it is respectfully submitted that the specification supports claim 5. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of no written description with regard to claim 5. Therefore, the written description rejection under 35 U.S.C. §112, first paragraph, of claim 5, and of claims 41, 7, 39, 25, 26, 11, 12-16, 17, 32, 18-20 and 34, which depend on claim 5, should be withdrawn.

7. The Specification Supports The Subject Matter of Group XVIII

Claim 27 is an independent claim directed to a process for detecting and/or identifying Trypanosoma cruzi in a biological sample. The process comprises: exposing DNA or RNA from the sample to a probe under such conditions that the probe hybridizes to a nucleotide sequence identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence; and detecting hybridization of the probe to said DNA or RNA to detect and/or identify Trypanosoma cruzi.

In arguing that this claim lacks written description, the Examiner argues for the first time in the October 3, 2003 Advisory Action that:

> Applicants "probe" does not recite any structure requirements. This simply leaves one of skill in the art to try to figure out what sequence of nucleotides, what length, what conditions of hybridization must be employed to practice the claim.

Although it is agreed that the exact sequence of the probe is not set forth in claim 27, it is respectfully submitted that the structure of the probe is not undefined. Instead, the structure of the probe is defined based on its ability to hybridize to a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence at the hybridization conditions used. From a review of the specification, particularly at page 18, lines 1-8; page 4, lines 7-18; page 6, lines 13-15; page 7, lines 5-19; page 15, lines 12-25; and page 16, lines 5-14, it is clear that the inventors were in possession of the invention of claim 27. In addition, there is nothing in the Eli Lilly line of cases that suggests that, in the context of a process claim, a probe cannot be defined based on the structure of the target sequence. In addition, there is nothing in these cases that suggest that the failure to identify hybridization

conditions in a process claim renders that claim lacking in written description. Thus, it is respectfully submitted that the Patent Office has provided no basis for a written description rejection of claim 27.

For at least these reasons, it is respectfully submitted that the specification supports claim 27. In addition, the Patent Office has not provided a *prima facie* basis to support a finding of no written description with regard to claim 27. Therefore, the written description rejection of claim 27 under 35 U.S.C. §112, first paragraph, should be withdrawn.

8. Conclusion

The present specification supports the subject matter of claims 5, 7, 8, 10-27, 32, 34 and 36-42. Therefore, the written description rejection under 35 U.S.C. §112, first paragraph, should be withdrawn.

D. Summary

Claims 5, 8, 10, 11, 17, 25, 26, 32, 34, 39 and 40 are not anticipated by Birkett. In addition, claims 5, 7, 8, 10-26, 32, 34 and 36-42 are enabled by the present specification. Furthermore, there is written description supporting claims 5, 7, 8, 10-27, 32, 34 and 36-42 in the present specification. Therefore, all of the pending rejections should be withdrawn and claim 5, 7, 8, 10-27, 32, 34 and 36-42 should be allowed, together with currently allowed claims 1 and 2.

VII. Conclusion

For all of the reasons discussed above, it is respectfully submitted that claims 5, 7, 8, 20-27, 32, 34 and 36-42 define patentable subject matter under 35 U.S.C. §102 and §112, first paragraph. Therefore, Appellants respectfully request this honorable Board to reverse the rejections of claims 5, 7, 8, 10-27, 32, 34 and 36-42.

Respectfully submitted,

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WPB:MLM/jam

Attachments:
Appendix A - Pending Claims
Appendix B - Groups of Rejected Claims

Date: November 20, 2003

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DEPOSIT ACCOUNT USE AUTHORIZATION
Please grant any extension necessary for entry;
Charge any fee due to our Deposit Account No. 15-0461

APPENDIX A
PENDING CLAIMS

CLAIMS:

1. A synthetic or isolated nucleic acid fragment which comprises a nucleotide sequence that is identical or fully complementary to a first sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence.

2. The nucleic acid fragment according to claim 1, wherein said nucleotide sequence is identical or fully complementary to a second sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.

5. A probe for identifying Trypanosoma cruzi, consisting essentially of a sequence having at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein said probe contains at least 5 and no more than 100 nucleotides.

7. The probe according to claim 5, wherein said probe has 8 to 50 nucleotides.

8. A primer for amplifying a nucleotide sequence, consisting essentially of a sequence having at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein said primer contains at least 5 and no more than 30 nucleotides.

10. The primer according to claim 8, wherein said primer consists essentially of a nucleotide sequence selected from the group consisting of SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10 and SEQ ID NO:12.

11. A reagent for detecting or identifying Trypanosoma cruzi in a biological sample, said reagent comprising a capture probe and a detection probe, both in accordance with claim 5, wherein said capture probe and said detection probe have nucleotide sequences that are different from one another.

12. The reagent according to claim 11, wherein said capture probe is attached to a solid support.

13. The reagent according to claim 12, wherein said capture probe is directly attached to said solid support.

14. The reagent according to claim 12, wherein said capture probe is indirectly attached to said solid support.

15. The reagent according to claim 11, wherein said detection probe is labeled by a marker selected from the group consisting of radioactive isotopes, enzymes capable of hydrolyzing a chromogenic, fluorigenic or luminescent substrate, chromophoric chemical compounds, fluorigenic compounds, luminescent compounds, nucleotide base analogs, and biotin.

16. The reagent according to claim 15, wherein said enzymes are selected from the group consisting of peroxidase and alkaline phosphatase.

17. The reagent according to claim 11, further comprising at least one primer consisting essentially of a segment of at least five contiguous nucleotides of a nucleic acid that is identical or fully complementary to a first sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence.

18. A method for detection and/or identification of Trypanosoma cruzi in a biological sample, comprising exposing denatured DNA extracted from Trypanosoma cruzi or DNA obtained by reverse transcription of RNA extracted from Trypanosoma cruzi to at least one probe according to claim 5; and detecting hybridization of said probe.

19. A method for detection and/or identification of Trypanosoma cruzi in a biological sample, comprising exposing extracted RNA from Trypanosoma cruzi to at least one probe according to claim 5; hybridizing said probe with said RNA; and detecting said hybridization.

20. The method according to claim 18, wherein before said DNA is exposed to said probe, said DNA is amplified in the presence of an enzymatic system with at least one primer, wherein said primer consists essentially of a segment of at least five contiguous nucleotides of a nucleic acid sequence that is identical or fully complementary to a sequence identified in SEQ ID NO: 1 or the corresponding RNA sequence.

21. A synthetic or isolated nucleic acid fragment that consists of a nucleotide sequence having at least 85% homology with a reference sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein each segment of 30 contiguous nucleotides of said nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of said reference sequence.

22. A synthetic or isolated nucleic acid fragment that consists of a nucleotide sequence having at least 85% homology with a reference sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein each segment of 30 contiguous nucleotides of said nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of said reference sequence.

23. A synthetic or isolated nucleic acid fragment that consists of a nucleotide sequence having at least 85% homology with a reference sequence that is identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein each segment of 30 contiguous

nucleotides of said nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of said reference sequence.

24. The nucleic acid fragment of claim 23, wherein said nucleotide sequence is identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.

25. A probe according to claim 5, wherein said nucleotide sequence is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence.

26. A probe according to claim 5, wherein said nucleotide sequence is identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.

27. A process for detecting and/or identifying Trypanosoma cruzi in a biological sample, comprising:

exposing DNA or RNA from the sample to a probe under such conditions that said probe hybridizes to a nucleotide sequence identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence; and

detecting hybridization of the probe to said DNA or RNA to detect and/or identify Trypanosoma cruzi.

32. The reagent of claim 17, wherein said primer contains no more than 30 nucleotides.

34. The method of claim 20, wherein said primer contains no more than 30 nucleotides.

36. The nucleic acid fragment of claim 21, wherein said nucleotide sequence:

is a nucleic acid sequence that is identical to or is a degenerate of a sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence, or

is a full complement of said nucleic acid sequence.

37. The nucleic acid fragment of claim 22, wherein said nucleotide sequence:

is a nucleic acid sequence that is identical to or is a degenerate of a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, or

is a full complement of said nucleic acid sequence.

38. The nucleic acid fragment of claim 23, wherein said nucleotide sequence:

is a nucleic acid sequence that is identical to or is a degenerate of a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, or

is a full complement of said nucleic acid sequence.

39. The probe of claim 5, wherein said probe contains at least five contiguous nucleotides of said nucleotide sequence.

40. The primer of claim 8, wherein said primer contains at least five contiguous nucleotides of said nucleotide sequence.

41. The probe according to claim 5, wherein said probe has 7 to 100 nucleotides.

42. The primer according to claim 8, wherein said primer has 7 to 30 nucleotides.

APPENDIX B
GROUPS OF REJECTED CLAIMS

Group I - Enablement, Written Description

21. A synthetic or isolated nucleic acid fragment that consists of a nucleotide sequence having at least 85% homology with a reference sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein each segment of 30 contiguous nucleotides of said nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of said reference sequence.

22. A synthetic or isolated nucleic acid fragment that consists of a nucleotide sequence having at least 85% homology with a reference sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein each segment of 30 contiguous nucleotides of said nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of said reference sequence.

23. A synthetic or isolated nucleic acid fragment that consists of a nucleotide sequence having at least 85% homology with a reference sequence that is identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein each segment of 30 contiguous nucleotides of said nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of said reference sequence.

Group II - Enablement, Written Description

36. The nucleic acid fragment of claim 21, wherein said nucleotide sequence:

is a nucleic acid sequence that is identical to or is a degenerate of a sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence, or

is a full complement of said nucleic acid sequence.

37. The nucleic acid fragment of claim 22, wherein said nucleotide sequence:

is a nucleic acid sequence that is identical to or is a degenerate of a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, or

is a full complement of said nucleic acid sequence.

38. The nucleic acid fragment of claim 23, wherein said nucleotide sequence:

is a nucleic acid sequence that is identical to or is a degenerate of a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, or

is a full complement of said nucleic acid sequence.

Group III - Enablement, Written Description

24. The nucleic acid fragment of claim 23, wherein said nucleotide sequence is identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.

Group IV - Enablement, Written Description, Art

8. A primer for amplifying a nucleotide sequence, consisting essentially of a sequence having at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at

nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein said primer contains at least 5 and no more than 30 nucleotides.

Group V - Enablement, Written Description

42. The primer according to claim 8, wherein said primer has 7 to 30 nucleotides.

Group VI - Enablement, Written Description, Art

40. The primer of claim 8, wherein said primer contains at least five contiguous nucleotides of said nucleotide sequence.

Group VII - Enablement, Written Description, Art

10. The primer according to claim 8, wherein said primer consists essentially of a nucleotide sequence selected from the group consisting of SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10 and SEQ ID NO:12.

Group VIII - Enablement, Written Description, Art

5. A probe for identifying Trypanosoma cruzi, consisting essentially of a sequence having at least 85% homology with a fragment of a nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein said probe contains at least 5 and no more than 100 nucleotides.

Group IX - Enablement, Written Description

41. The probe according to claim 5, wherein said probe has 7 to 100 nucleotides.

7. The probe according to claim 5, wherein said probe has 8 to 50 nucleotides.

Group X - Enablement, Written Description, Art

39. The probe of claim 5, wherein said probe contains at least five contiguous nucleotides of said nucleotide sequence.

Group XI - Enablement, Written Description, Art

25. A probe according to claim 5, wherein said nucleotide sequence is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence.

Group XII - Enablement, Written Description, Art

26. A probe according to claim 5, wherein said nucleotide sequence is identical or fully complementary to a sequence starting at nucleotide 1266 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence.

Group XIII - Enablement, Written Description, Art

11. A reagent for detecting or identifying Trypanosoma cruzi in a biological sample, said reagent comprising a capture probe and a detection probe, both in accordance with claim 5, wherein said capture probe and said detection probe have nucleotide sequences that are different from one another.

Group XIV - Enablement, Written Description

12. The reagent according to claim 11, wherein said capture probe is attached to a solid support.

13. The reagent according to claim 12, wherein said capture probe is directly attached to said solid support.

14. The reagent according to claim 12, wherein said capture probe is indirectly attached to said solid support.

15. The reagent according to claim 11, wherein said detection probe is labelled by a marker selected from the group consisting of radioactive isotopes, enzymes capable of hydrolyzing a chromogenic, fluorigenic or luminescent substrate, chromophoric chemical compounds, fluorigenic compounds, luminescent compounds, nucleotide base analogs, and biotin.

16. The reagent according to claim 15, wherein said enzymes are selected from the group consisting of peroxidase and alkaline phosphatase.

Group XV - Enablement, Written Description, Art

17. The reagent according to claim 11, further comprising at least one primer consisting essentially of a segment of at least five contiguous nucleotides of a nucleic acid that is identical or fully complementary to a first sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence.

32. The reagent of claim 17, wherein said primer contains no more than 30 nucleotides.

Group XVI - Enablement, Written Description

18. A method for detection and/or identification of Trypanosoma cruzi in a biological sample, comprising exposing denatured DNA extracted from Trypanosoma cruzi or DNA obtained by reverse transcription of RNA extracted from Trypanosoma cruzi to at least one probe according to claim 5; and detecting hybridization of said probe.

19. A method for detection and/or identification of Trypanosoma cruzi in a biological sample, comprising exposing extracted RNA from Trypanosoma cruzi to at least one probe according to claim 5; hybridizing said probe with said RNA; and detecting said hybridization.

20. The method according to claim 18, wherein before said DNA is exposed to said probe, said DNA is amplified in the presence of an enzymatic system with at least one primer, wherein said primer consists essentially of a segment of at least five contiguous nucleotides of a nucleic acid sequence that is identical or fully complementary to a sequence identified in SEQ ID NO: 1 or the corresponding RNA sequence.

Group XVII - Enablement, Written Description, Art

34. The method of claim 20, wherein said primer contains no more than 30 nucleotides.

Group XVIII - Written Description

27. A process for detecting and/or identifying Trypanosoma cruzi in a biological sample, comprising:

exposing DNA or RNA from the sample to a probe under such conditions that said probe hybridizes to a nucleotide sequence identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence; and

detecting hybridization of the probe to said DNA or RNA to detect and/or identify Trypanosoma cruzi.